

Serial Number: 09/733,685

CRF Processing Date: 12/21/2000
 Edited by: *Ar*
 Verified by: *Ar* (STIC staff)

ENTERED

#2
 0430
 3/27/01

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☒ Other: *Seq 22-23 - inserted hard returns*

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form. 3/1/95

OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/733,685

DATE: 12/21/2000
 TIME: 10:14:24

Input Set : A:\seq-list.txt
 Output Set: N:\CRF3\12212000\I733685.raw

Does Not Comply
 Corrected Diskette Needed

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3 <110> APPLICANT: Cade, Rebecca M
4   Dietrich, Robert A
6 <120> TITLE OF INVENTION: GENES ENCODING PROTEINS INVOLVED IN THE REGULATION OF
7   SAR GENE EXPRESSION IN PLANTS
9 <130> FILE REFERENCE: A-31089A
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/733,685
C--> 12 <141> CURRENT FILING DATE: 2000-12-08
14 <150> PRIOR APPLICATION NUMBER: 60/171,008
15 <151> PRIOR FILING DATE: 1999-12-15
17 <150> PRIOR APPLICATION NUMBER: 60/175,519
18 <151> PRIOR FILING DATE: 2000-01-11
20 <160> NUMBER OF SEQ ID NOS: 23
22 <170> SOFTWARE: PatentIn Ver. 2.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 509
26 <212> TYPE: DNA
27 <213> ORGANISM: Arabidopsis thaliana
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31 <222> LOCATION: (68)..(433)
32 <223> OTHER INFORMATION: gene product NI16
34 <220> FEATURE:
35 <221> NAME/KEY: misc_feature
36 <222> LOCATION: (142)..(147)
37 <223> OTHER INFORMATION: SalI site
39 <220> FEATURE:
40 <221> NAME/KEY: misc_feature
41 <222> LOCATION: (344)..(349)
42 <223> OTHER INFORMATION: EcoRI site
44 <400> SEQUENCE: 1
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47 ggctaac atg aac aac tct ttg aag aaa gaa gaa cgc gta gaa gaa gat 109
48   Met Asn Asn Ser Leu Lys Lys Glu Glu Arg Val Glu Glu Asp
49   1             5             10
51 aac gga aaa tct gac ggt aac aga ggg aaa ccg tcg acg gaa gtt gtt 157
52 Asn Gly Lys Ser Asp Gly Asn Arg Gly Lys Pro Ser Thr Glu Val Val
53 15             20             25             30
55 cgg acg gta acg gag gaa gag gtg gat gag ttt ttc aag ata tta cgg 205
56 Arg Thr Val Thr Glu Glu Glu Val Asp Glu Phe Phe Lys Ile Leu Arg
57             35             40             45
59 aga gta cac gtg gcg aca cga acg gtt gcg aaa gtt aac ggc ggt gtt 253
60 Arg Val His Val Ala Thr Arg Thr Val Ala Lys Val Asn Gly Gly Val
61             50             55             60
63 gct gag gga gag tta ccg tct aag aag agg aaa cgg agt cag aat ctt 301
64 Ala Glu Gly Glu Leu Pro Ser Lys Lys Arg Lys Arg Ser Gln Asn Leu
65             65             70             75
67 ggg ttg aga aac tcg ttg gat tgt aac ggc gtt cga gac gga gaa ttc 349

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 PATENT APPLICATION: US/09/733,685 TIME: 10:14:24

Input Set : A:\seq-list.txt
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68 Gly Leu Arg Asn Ser Leu Asp Cys Asn Gly Val Arg Asp Gly Glu Phe
69      80                      85                      90
71 gat gag att aat cag gtc ggg tta caa ggt ttg ggt ttg gat ctg aac   397
72 Asp Glu Ile Asn Arg Val Gly Leu Gln Gly Leu Gly Leu Asp Leu Asn
73  95                      100                      105                      110
75 tgt aaa ccg gaa cca gac agc gtt agt tta tca ttg tagacttgta   443
76 Cys Lys Pro Glu Pro Asp Ser Val Ser Leu Ser Leu
77      115                      120
79 gtcttctcatg tttttccct tcttacaata atcaattttt ttttaactac aatacttttg 503
81 aaaaaa   509
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85 <211> LENGTH: 122
86 <212> TYPE: PRT
87 <213> ORGANISM: Arabidopsis thaliana
89 <400> SEQUENCE: 2
90 Met Asn Asn Ser Leu Lys Lys Glu Glu Arg Val Glu Glu Asp Asn Gly
91  1      5      10      15
93 Lys Ser Asp Gly Asn Arg Gly Lys Pro Ser Thr Glu Val Val Arg Thr
94      20      25      30
96 Val Thr Glu Glu Glu Val Asp Glu Phe Phe Lys Ile Leu Arg Arg Val
97      35      40      45
99 His Val Ala Thr Arg Thr Val Ala Lys Val Asn Gly Gly Val Ala Glu
100     50      55      60
102 Gly Glu Leu Pro Ser Lys Lys Arg Lys Arg Ser Gln Asn Leu Gly Leu
103  65      70      75      80
105 Arg Asn Ser Leu Asp Cys Asn Gly Val Arg Asp Gly Glu Phe Asp Glu
106      85      90      95
108 Ile Asn Arg Val Gly Leu Gln Gly Leu Gly Leu Asp Leu Asn Cys Lys
109     100     105     110
111 Pro Glu Pro Asp Ser Val Ser Leu Ser Leu
112     115     120
116 <210> SEQ ID NO: 3
117 <211> LENGTH: 1700
118 <212> TYPE: DNA
119 <213> ORGANISM: Arabidopsis thaliana
121 <220> FEATURE:
122 <221> NAME/KEY: misc_feature
123 <222> LOCATION: (365)..(374)
124 <223> OTHER INFORMATION: TCA1 motif
126 <220> FEATURE:
127 <221> NAME/KEY: misc_feature
128 <222> LOCATION: (426)..(435)
129 <223> OTHER INFORMATION: TCA1 motif
131 <220> FEATURE:
132 <221> NAME/KEY: misc_feature
133 <222> LOCATION: (609)..(614)
134 <223> OTHER INFORMATION: MYCATR22 element
136 <220> FEATURE:
137 <221> NAME/KEY: misc_feature

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RAW SEQUENCE LISTING
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Input Set : A:\seq-list.txt
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138 <222> LOCATION: (646)..(665)
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144 <223> OTHER INFORMATION: L BOX
146 <220> FEATURE:
147 <221> NAME/KEY: misc_feature
148 <222> LOCATION: (757)..(762)
149 <223> OTHER INFORMATION: HEXAMERAT 4 element
151 <220> FEATURE:
152 <221> NAME/KEY: misc_feature
153 <222> LOCATION: (863)..(1228)
154 <223> OTHER INFORMATION: NI16 genomic coding region
156 <400> SEQUENCE: 3
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158 catgacaaat attaatatat cagtgttaaat aacatgtttt qttcttaaaa tacatgcatt 120
159 ttaaaatlcag acatttgttt taaaatcaaa tctaattctt tatatcacia cgaattlgac 180
160 ggaatttca ggtaaaaaga gaaatataag aatgagagat agagagattt ctatqgaaaa 240
161 aqaaaagag aacatgtaag tgacaaatat aaagagatat gatgatatat ttatqagag 300
162 tgggtgaaga tttttttagg agagggagag aqaatagaa aaaaaaatg acatggtgaa 360
163 tctgaagaag atgaatttgt ttaagatga agagagaaag agaactccat ggctaaagtc 420
164 tctgaagaag gatgaataag aacaaaga aggaagaaga aagagaaagg ctaaaataga 480
165 ctactattg ccaaaatttc tgtagccgac aaatactatt tggctccagg ttattttgtg 540
166 tattcttttg aaqtcaaaag ttatttctta catatactct aaaaatatag ccgataccaa 600
167 ttttccaca catggacttc ctttattcca aaagtcaata aagtgtgacg tcatgatact 660
168 tacgtttta aacatcgcat gatgatgtca tttagcataa tctccaccgt ccaattlatt 720
169 tagttgttg caatatcgac cgtctaaqtt ccacaccgac ggctataaga gtttcattat 780
170 aatttttagc aaaaataaat cagcaataaa tttttcttg actaaqctta aacgacgccc 840
171 ttaacatttt cttctggtta acatgaacaa ctctttgaag aaagaagaac gcgtagaaga 900
172 agataacgga aaatctgacg qtaacagagg gaaaccgtcg acggaagtig ttcgacggt 960
173 aacggaaggaa gagggtgatg agtttttcaa qatattacgg aqagtacacg tggcgacacg 1020
174 aacggttgcg aaagttaacg gcygtgttgc tgaaggagag ttaccgtcta agaagaggaa 1080
175 acggagtcag aatcttgggt tgagaaactc gttggattgt aacggcgttc gagacggaga 1140
176 attcgatgag attaatcggg tcgggttaca ggggttgggt ttggtctga actgtaaac 1200
177 ggaaccagac agcgttagtt tatcgttqta gacttqtagt ccttcattgt tttcccttc 1260
178 ttacaataat caattttttt ttaactacaa taacttttga aaaaatggtt aaagaagatt 1320
179 attaacatgt tatccaaatt tcagattcct caqttttatt ttatacgtca aaagaagaat 1380
180 tatatatttg caaaactaca agtcaaacaa aagctattta agcgtttgac gttcctaaac 1440
181 aacataaatt ttaactaaat caatgtttta aaaaagtgtt gatggtaaag atatcaattg 1500
182 ggccctttgc tggcccggtt agtaalatlg cagagtaggt atggccctgt ataagggaat 1560
183 ccaaaaaaag agcgggcatt gcgggttggg tgcgtttgga actttggatt gtggttagt 1620
184 catggtttat ctattaatgt ctgcggactt gtggaacgag cgtttgttct tcttctctg 1680
185 tttacgactt acgaacatat
188 <210> SEQ ID NO: 4
189 <211> LENGTH: 608
190 <212> TYPE: DNA
191 <213> ORGANISM: Solanum tuberosum
193 <220> FEATURE:
  
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194 <221> NAME/KEY: CDS
195 <222> LOCATION: (124)..(438)
197 <400> SEQUENCE: 4
198 caggttatgc acacagaasa cattgacata acagatrgaa tacacattat attatattaa 50
200 tgagagaata aagagaagta attgcactag cagtattgac aattaatcag ctagecggct 120
202 tga atg cta ctt atg gac gga gaa aag aag agy aag aga aca gca atc 168
203 Met Leu Leu Met Asp Gly Glu Lys Lys Arg Lys Arg Thr Ala Ile
204 1 5 10 15
206 ggc gcc gga gat ccg agt aag gat gag gta gaa gct act gtg aag gag 216
207 Gly Ala Gly Asp Arg Ser Lys Asp Glu Val Glu Ala Thr Val Lys Glu
208 20 25 30
210 gag gag ccg ccg tca gag gcc gag gtt qac gag ttc ttc gcc atc tta 264
211 Glu Glu Pro Pro Ser Glu Ala Glu Val Asp Glu Phe Phe Ala Ile Leu
212 35 40 45
214 ccg agg atg cat gtg gcc gtg aaa tal ctc cag aga aat gct cag att 312
215 Arg Arg Met His Val Ala Val Lys Tyr Leu Gln Arg Asn Ala Glu Ile
216 50 55 60
218 ccg ccg qaa aac ctt aac qca tcg ccg gcc ggt gct aac ggt gtc qca 360
219 Arg Pro Glu Asn Leu Asn Ala Ser Pro Ala Gly Ala Asn Gly Val Ala
220 65 70 75
222 gct gga ccg aag aga qaa ccg qga atc gtg aga aaa ggt gat ttg gac 408
223 Ala Gly Arg Lys Arg Glu Arg Gly Ile Val Arg Lys Gly Asp Leu Asp
224 80 85 90 95
226 ctc aac act ctg ccg qac gcc qga gac taa ttaacgcagt ttaagcatag 458
227 Leu Asn Thr Leu Pro Asp Gly Gly Asp
W--> 228 100 105
230 gtttaattaca taaatgcacc ctttaattalc ctageattctt aagattgac tgcctgtacag 518
232 attaattaat taaagccttt ttttatatat atttctccg taaacgggtt gctctttgtg 578
234 attttcttta ataaatttaa tttattttat 608
237 <210> SEQ ID NO: 5
238 <211> LENGTH: 104
239 <212> TYPE: PRT
240 <213> ORGANISM: Solanum tuberosum
242 <400> SEQUENCE: 5
243 Met Leu Leu Met Asp Gly Glu Lys Lys Arg Lys Arg Thr Ala Ile Gly
244 1 5 10 15
245 Ala Gly Asp Arg Ser Lys Asp Glu Val Glu Ala Thr Val Lys Glu Glu
246 20 25 30
247 Glu Pro Pro Ser Glu Ala Glu Val Asp Glu Phe Phe Ala Ile Leu Arg
248 35 40 45
249 Arg Met His Val Ala Val Lys Tyr Leu Gln Arg Asn Ala Gln Ile Arg
250 50 55 60
251 Pro Glu Asn Leu Asn Ala Ser Pro Ala Gly Ala Asn Gly Val Ala Ala
252 65 70 75 80
253 Gly Arg Lys Arg Glu Arg Gly Ile Val Arg Lys Gly Asp Leu Asp Leu
254 85 90 95
255 Asn Thr Leu Pro Asp Gly Gly Asp
256 100
260 <210> SEQ ID NO: 6

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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/733,685

DATE: 12/21/2000
 TIME: 10:14:24

Input Set : A:\seq-list.txt
 Output Set: N:\CRF3\12212000\I733685.raw

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261 <211> LENGTH: 349
262 <212> TYPE: DNA
263 <213> ORGANISM: Lycopersicon esculentum
265 <220> FEATURE:
266 <221> NAME/KEY: CDS
267 <222> LOCATION: (3)..(233)
269 <400> SEQUENCE: 6
270 ct tcg qag gga gag gtg gat qag ttt ttc gca att tta cgg agg atg 47
271 Ser Glu Gly Glu Val Asp Glu Phe Phe Ala ile Leu Arg Arg Met
272 1 5 10 15
274 cgc atg gcc gla aaa tat ctt caa aga aac qct cag att cag ccg gaa 93
275 His Met Ala Val Lys Tyr Leu Gln Arg Asn Ala Gln ile Glu Pro Glu
276 20 25 30
278 aac gtt aac gct cac ggc agc aag tta acc gca tcg ccg gcc ggt gtt 143
279 Asn Val Asn Ala His Gly Ser Lys Leu Thr Ala Ser Pro Ala Gly Val
280 35 40 45
282 aac gga gat gca act gga cag aag aga gaa cgg gga atc gtg aga aaa 191
283 Asn Gly Asp Ala Thr Gly Gln Lys Arg Glu Arg Gly ile Val Arg Lys
284 50 55 60
286 ggt gat ttg gac ctg aac act ttg ccg gac tgc qga gac taa 233
287 Gly Asp Leu Asp Leu Asn Thr Leu Pro Asp Cys Gly Asp
288 65 70 75
290 cgcagtttaa gcataggtta attacagaaa tgcaccttta attatcgtag attcttaaga 293
292 ttgactgtct gtacaaaatta attaaatgaa gcttlttttt atatataaaa aaaaaa 349
295 <210> SEQ ID NO: 7
296 <211> LENGTH: 76
297 <212> TYPE: PRT
298 <213> ORGANISM: Lycopersicon esculentum
300 <400> SEQUENCE: 7
301 Ser Glu Gly Glu Val Asp Glu Phe Phe Ala ile Leu Arg Arg Met His
302 1 5 10 15
303 Met Ala Val Lys Tyr Leu Gln Arg Asn Ala Gln ile Glu Pro Glu Asn
304 20 25 30
305 Val Asn Ala His Gly Ser Lys Leu Thr Ala Ser Pro Ala Gly Val Asn
306 35 40 45
307 Gly Asp Ala Thr Gly Gln Lys Arg Glu Arg Gly ile Val Arg Lys Gly
308 50 55 60
309 Asp Leu Asp Leu Asn Thr Leu Pro Asp Cys Gly Asp
310 65 70 75
314 <210> SEQ ID NO: 8
315 <211> LENGTH: 75
316 <212> TYPE: PRT
317 <213> ORGANISM: Glycine max
319 <400> SEQUENCE: 8
320 Met Glu Val Glu Lys Arg Lys Asn Lys Arg Val Met Gly Glu Glu Glu
321 1 5 10 15
323 Glu Ser Glu Arg Val Lys Asn Lys Arg Leu Lys Gly Val Glu Glu Glu
324 20 25 30
326 Asp Gly Ser Asp Gly Val Pro Thr Glu Glu Glu Val Glu Glu Phe Phe

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VERIFICATION SUMMARY DATE: 12/21/2000
PATENT APPLICATION: US/09/733,685 TIME: 10:14:25

Input Set : A:\seq-list.txt
Output Set: N:\CRF3\12212000\I733685.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:228 M:336 W: Invalid Amino Acid Number in Coding Region, Seq ID:4
L:512 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:530 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:534 M:283 W: Missing Blank Line separator, <220> field identifier
L:534 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:535 M:282 W: Numeric Field Identifier Missing, <211> is required.
L:535 M:282 W: Numeric Field Identifier Missing, <212> is required.
L:535 M:282 W: Numeric Field Identifier Missing, <213> is required.
L:535 M:283 W: Missing Blank Line separator, <400> field identifier
L:570 M:282 W: Numeric Field Identifier Missing, <211> is required.
L:570 M:282 W: Numeric Field Identifier Missing, <212> is required.
L:570 M:282 W: Numeric Field Identifier Missing, <213> is required.
L:570 M:283 W: Missing Blank Line separator, <400> field identifier